

09/596,746.

PATENT APPLICATION  
Attorney's Docket No.: 2631.1002-001



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Raymond J. Dattwyler, Gerald Seinost, Daniel Dykhuizen, Benjamin J. Luft,  
Maria J.C. Gomes-Solecki

C 8 C  
EME

Issued: June 13, 2006

Patent No.: 7,060,281 B1

Title: GROUPS OF BORRELIA BURGDORFERI AND BORRELIA AFZELII  
THAT CAUSE LYME DISEASE IN HUMANS

CERTIFICATE OF MAILING OR TRANSMISSION

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6/22/07

Date

Katie Norris

Signature

Katie Norris

Typed or printed name of person signing certificate

REQUEST FOR CERTIFICATE OF CORRECTION

Office of Publications  
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Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

Pursuant to 35 U.S.C. § 254, we hereby request a Certificate of Correction be issued for the above-referenced U.S. Letters Patent for the following reasons:

SEQ ID NOS. 53-86 were not included in the issued patent, even though they were properly entered in a Substitute Sequence Listing filed on September 22, 2005. Certain of the claims recite SEQ ID NOs that are not in the published patent, which will be confusing for the public.

Certificate  
JUN 28 2007  
of Correction

Since the errors were made by the U.S. Patent and Trademark Office and not by Patentees or Patentee's Attorney/Agent, it is understood that there are no additional fees for the requested Certificate of Correction. A Certificate of Correction is enclosed herewith.

Respectfully submitted,

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By Doreen M. Hough Reg. No. 36,361/for  
Elizabeth W. Mata  
Registration No.: 38,236  
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Facsimile: (978) 341-0136

Concord, MA 01742-9133

Dated: June 22, 2007

UNITED STATES PATENT AND TRADEMARK OFFICE  
**CERTIFICATE OF CORRECTION****PATENT NO. : 7,060,281 B1****DATED : June 13, 2006****INVENTOR(S) : Raymond J. Dattwyler, Gerald Steinost, Daniel  
Dykhuizen, Benjamin J. Luft, Maria J.C. Gomes-Solecki**

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

**At Column 45, Insert SEQ ID NOS. 53-86 after SEQ ID NO: 52**

&lt;210&gt; 53

&lt;211&gt; 1137

&lt;212&gt; DNA

&lt;213&gt; ospC Chimera

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1137)

&lt;400&gt; 53

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530 Virginia Road, P.O. Box 9133  
Concord, Massachusetts 01742-9133PATENT NO. 7,060,281 B1No. of add'l copies  
@ 50¢ per page



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<213> ospC Chimera	
<400> 58	
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
1 5 10 15	
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
35 40 45	
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
50 55 60	
Ile Asp Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser	
65 70 75 80	
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
85 90 95	
Ser Lys Leu Lys Asn Leu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
100 105 110	
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
115 120 125	
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
130 135 140	

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Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
145 150 155 160  
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
165 170 175  
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro  
180 185 190  
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
195 200 205  
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
210 215 220  
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
225 230 235 240  
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
245 250 255  
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
260 265 270  
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
275 280 285  
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys  
290 295 300  
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
305 310 315 320  
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
325 330 335  
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
340 345 350  
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
355 360 365  
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
370 375 380  
Lys Pro  
385

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<210> 59  
 <211> 1197  
 <212> DNA  
 <213> ospC Chimera  
  
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 <221> CDS  
 <222> (1)....(1197)  
  
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Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys		
1		5						10					15				

  

gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa		96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys		
		20						25					30				

  

gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct		144
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro		
		35				40						45					

  

aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gcg	gtt	tta		192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu		
		50				55						60					

  

ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	ttg	ctg	tca	tct	ata	gat	gaa	att		240
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile		
		65			70					75			80				

  

gct	gct	aaa	gct	att	ggt	aaa	aaa	ata	cac	caa	aat	aat	ggt	ttg	gat		288
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp		
								85		90			95				

  

acc	gaa	tat	aat	cac	aat	gga	tca	ttg	tta	gcg	gga	gct	tat	gca	ata		336
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile		
					100			105				110					

  

tca	acc	cta	ata	aaa	caa	aaa	tta	gat	gga	ttg	aaa	aat	gaa	gga	tta		384
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu		
		115					120					125					

  

aag	gaa	aaa	att	gat	gcg	gct	aag	aaa	tgt	tct	gaa	aca	ttt	act	aat		432
Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn		
							130			135		140					

  

aaa	tta	aaa	gaa	aaa	cac	aca	gat	ctt	ggt	aaa	gaa	ggt	gtt	act	gat		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

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Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp				
145	150	155	160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa				528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys				
165	170	175		
ggc gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca				576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser				
180	185	190		
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc				624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser				
195	200	205		
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat				672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp				
210	215	220		
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat				720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn				
225	230	235	240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc				768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu				
245	250	255		
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct				816
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala				
260	265	270		
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag				864
Lys Ala Ile Gly Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu				
275	280	285		
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac				912
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn				
290	295	300		
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag				960
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys				
305	310	315	320	
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa				1008
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys				
325	330	335		

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tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056  
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
 340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
 355 360 365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152  
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
 370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197  
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390 395

<210> 60  
<211> 399  
<212> PRT  
<213> ospC Chimera

<400> 60  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190

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Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
     195                  200                  205  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
     210                  215                  220  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
     225                  230                  235                  240  
  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
     245                  250                  255  
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala  
     260                  265                  270  
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu  
     275                  280                  285  
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn  
     290                  295                  300  
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys  
     305                  310                  315                  320  
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys  
     325                  330                  335  
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
     340                  345                  350  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
     355                  360                  365  
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
     370                  375                  380  
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
     385                  390                  395

<210> 61  
 <211> 1196  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1196)

<400> 61  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt    48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
     1                  5                  10                  15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa    96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
     20                  25                  30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35	40
	45
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50	55
	60
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65	70
	75
65	80
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85	90
	95
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100	105
	110
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115	120
	125
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130	135
	140
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145	150
	155
	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165	170
	175
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180	185
	190
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195	200
	205
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210	215
	220

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ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225	230
230	235
235	240
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245	250
250	255
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct	816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
260	265
265	270
270	275
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc	864
Thr Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu Ala Val	
275	280
280	285
285	290
290	295
295	300
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca	912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
290	295
295	300
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta	960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu	
305	310
310	315
315	320
320	325
325	330
330	335
335	340
340	345
345	350
350	355
355	360
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790	795
795	800
800	805
805	810
810	815
815	820
820	825
825	830
830	835
835	840
840	845
845	850
850	855
855	860
860	865
865	870
870	875
875	880
880	885
885	890
890	895
895	900
900	905
905	910
910	915
915	920
920	925
925	930
930	935
935	940
940	945
945	950
950	955
955	960
960	965
965	970
970	975
975	980
980	985
985	990
990	995
995	1000

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<210> 62  
<211> 398  
<212> PRT  
<213> ospC Chimera

<400> 62  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80  
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
210 215 220  
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
225 230 235 240  
Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
245 250 255  
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
260 265 270  
Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val  
275 280 285  
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
290 295 300  
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu  
305 310 315 320

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Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys  
                  325                 330                 335  
  
 Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp  
                  340                 345                 350  
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys  
                  355                 360                 365  
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala  
                  370                 375                 380  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
                  385                 390                 395

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<210> 63  
<211> 1185  
<212> DNA  
<213> ospC Chimera
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<220>  
<221> CDS  
<222> (1) . . . (1185)

<400> 63  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

```

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
          20           25           30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt.aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
                   35                  40                  45

```

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
      50           55           60

```

```

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt      240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
   65           70           75           80

```

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta"tat aat 288  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser 100 105 110	336
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu 115 120 125	384
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr 130 135 140	432
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp 145 150 155 160	480
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp 165 170 175	528
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu 180 185 190	576
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser 210 215 220	672
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly 260 265 270	816
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac	864
	7,060,281 B1

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Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn			
275	280	285	
gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa			912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys			
290	295	300	
aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa			960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu			
305	310	315	320
aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa			1008
Lys Ala Lys Lys Cys Ser Gly Glu Phe Thr Ala Lys Leu Lys Gly Glu			
325	330	335	
cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa			1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys			
340	345	350	
gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt			1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu			
355	360	365	
gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag			1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu			
370	375	380	
atg ctt act aat tca gtt aaa gag ctt aca agc			1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser			
385	390	395	

<210> 64  
<211> 395  
<212> PRT  
<213> ospC Chimera

<400> 64  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
1               5               10               15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20               25               30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35               40               45  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50               55               60

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Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65                   70                   75                   80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85                   90                   95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 100                 105                 110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
 115                 120                 125  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
 130                 135                 140  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
 145                 150                 155                 160  
 Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
 165                 170                 175  
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
 180                 185                 190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
 195                 200                 205  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
 210                 215                 220  
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
 225                 230                 235                 240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
 245                 250                 255  
 Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly  
 260                 265                 270  
 Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn  
 275                 280                 285  
 Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys  
 290                 295                 300  
 Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu  
 305                 310                 315                 320  
 Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu  
 325                 330                 335  
 His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys  
 340                 345                 350  
 Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu  
 355                 360                 365  
 Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu  
 370                 375                 380  
 Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385                 390                 395

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<210> 65  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera  
  
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 <221> CDS  
 <222> (1) ... (1184)  
  
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 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65 70 75 80  
  
 gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95  
  
 gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 100 105 110  
  
 acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
 115 120 125  
  
 aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
 130 135 140  
  
 aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480

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Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat			528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta			576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu			
180	185	190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca			624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr			
195	200	205	
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct			672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser			
210	215	220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata			720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile			
225	230	235	240
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa			768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu			
245	250	255	
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att			816
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile			
260	265	270	
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat			864
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His			
275	280	285	
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca			912
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr			
290	295	300	
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att			960
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile			
305	310	315	320
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga			1008
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly			
325	330	335	

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gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa		1056	
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys			
340	345	350	
aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag		1104	
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu			
355	360	365	
ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa		1152	
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys			
370	375	380	
gag atg ctt gct aat tca gtt aaa gag ctt ac		1184	
Glu Met Leu Ala Asn Ser Val Lys Glu Leu			
385	390		
<210> 66			
<211> 394			
<212> PRT			
<213> ospC Chimera			
<400> 66			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu			
65	70	75	80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn			
85	90	95	
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser			
100	105	110	
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu			
115	120	125	
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr			
130	135	140	
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	

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Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
     180                        185                        190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
     195                        200                        205  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
     210                        215                        220  
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
     225                        230                        235                        240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
     245                        250                        255  
 Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
     260                        265                        270  
 Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His  
     275                        280                        285  
 Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr  
     290                        295                        300  
 Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile  
     305                        310                        315                        320  
 Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly  
     325                        330                        335  
 Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys  
     340                        345                        350  
 Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu  
     355                        360                        365  
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys  
     370                        375                        380  
 Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
     385                        390

<210> 67  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1184)

<400> 67  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt     48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
     1                      5                             10                     15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa     96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
     20                      25                             30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 .	40
45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50	55
55	60
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65	70
75	80
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85	90
90	95
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100	105
105	110
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115	120
120	125
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130	135
135	140
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145	150
150	155
155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165	170
170	175
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180	185
185	190
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195	200
200	205

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agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser	
210	215
220	
aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225	230
235	240
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245	250
255	
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att	816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
260	265
270	
ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac	864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn	
275	280
285	
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa	912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu	
290	295
300	
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca	960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr	
305	310
315	320
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat	1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His	
325	330
335	
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct	1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala	
340	345
350	
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa	1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355	360
365	
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr	
370	375
380	
tta aaa aat gct gtt aaa gag ctt aca agt cc	1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser	
385	390

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<210> 68  
 <211> 394  
 <212> PRT  
 <213> ospC Chimera

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
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 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
   20                 25                  30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
   35                 40                  45  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
   50                 55                  60  
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu  
   65                 70                  75                  80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
   85                 90                  95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
   100                105                110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
   115                120                125  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
   130                135                140

Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
   145                150                155                  160  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
   165                170                175  
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
   180                185                190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
   195                200                205  
 Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
   210                215                220  
 Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
   225                230                235                  240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
   245                250                255  
 Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
   260                265                270  
 Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn  
   275                280                285  
 Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu  
   290                295                300

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Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr  
 305               310               315               320  
 Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His  
              325               330               335  
 Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala  
              340               345               350  
 Ile Leu Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu  
              355               360               365  
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr  
              370               375               380  
 Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
 385               390

<210> 69  
<211> 1209  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1209)

<400> 69  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1               5               10               15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa   96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20               25               30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct   144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35               40               45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta   192  
Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50               55               60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt   240  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65               70               75               80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat   288  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85               90               95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100	105
	110
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115	120
	125
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130	135
	140
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145	150
	155
	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165	170
	175
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180	185
	190
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195	200
	205
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
210	215
	220
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
225	230
	235
	240
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
245	250
	255
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
260	265
	270

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ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser 275 280 285	864
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu 290 295 300	912
agt gta ttg aat tca gaa gaa tta aag aaa att aaa gag gct aag Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys 305 310 315 320	960
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu 325 330 335	1008
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu 340 345 350	1056
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu 355 360 365	1104
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr 370 375 380	1152
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys 385 390 395 400	1200
aaa cct taa Lys Pro *	1209

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<212> PRT  
<213> ospC Chimera

<400> 70  
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1 5 10 15  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

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Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
     35                        40                        45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
     50                        55                        60  
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu  
     65                        70                        75                        80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
     85                        90                        95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
     100                       105                       110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
     115                       120                       125  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
     130                       135                       140  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
     145                       150                       155                       160  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
     165                       170                       175  
 Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
     180                       185                       190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
     195                       200                       205  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
     210                       215                       220  
 Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
     225                       230                       235                       240  
 Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
     245                       250                       255  
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
     260                       265                       270  
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
     275                       280                       285  
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
     290                       295                       300  
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys  
     305                       310                       315                       320  
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
     325                       330                       335  
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
     340                       345                       350  
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
     355                       360                       365  
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
     370                       375                       380  
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
     385                       390                       395                       400  
 Lys Pro

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<211> 1179
<212> DNA
<213> ospC Chimera

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1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
130 135 140

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ctt aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat		480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp		
145	150	155
		160
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt		528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly		
165	170	175
gct gca gaa ctt gaa aag tta ttt aaa gct gta gaa aac tta tca aaa		576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys		
180	185	190
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct		624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro		
195	200	205
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat		672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn		
210	215	220
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa		720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys		
225	230	235
		240
aaa att aca gaa tct aac gca gtt ctt ctc gcc gtg aaa gaa gtt gaa		768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu		
245	250	255
act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa		816
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys		
260	265	270
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca		864
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser		
275	280	285
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata		912
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile		
290	295	300
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct		960
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala		
305	310	315
		320
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca		1008
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr		
325	330	335

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gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056  
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
 340 345 350

tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104  
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
 355 360 365

tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152  
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
 370 375 380

act aat tca gtt aaa gag ctt aca agc 1179  
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 385 390

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 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85 90 95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100 105 110  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115 120 125  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130 135 140  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145 150 155 160  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165 170 175

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Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
     180                     185                     190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
     195                     200                     205  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
     210                     215                     220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
     225                     230                     235                     240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
     245                     250                     255  
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys  
     260                     265                     270  
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser  
     275                     280                     285  
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile  
     290                     295                     300  
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala  
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 Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr  
     325                     330                     335  
  
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
     340                     345                     350  
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
     355                     360                     365  
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 Thr Asn Ser Val Lys Glu Leu Thr Ser  
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  1                     5                             10                     15

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 Concord, Massachusetts 01742-9133

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	96		
20	25	30	
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	144		
35	40	45	
 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	192		
50	55	60	
 ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	240		
65	70	75	80
 gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala	288		
85	90	95	
 aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	336		
100	105	110	
 gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	384		
115	120	125	
 gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	432		
130	135	140	
 cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	480		
145	150	155	160
 aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	528		
165	170	175	
 gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	576		
180	185	190	
 gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	624		
195	200	205	

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att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat		672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn		
210	215	220
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa		720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys		
225	230	235
240		
aaa att aca gaa tct aac gca gtt ctg gct gtg aaa gaa att gaa		768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu		
245	250	255
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa		816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys		
260	265	270
aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga		864
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly		
275	280	285
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa		912
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys		
290	295	300
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat		960
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn		
305	310	315
320		
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat		1008
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His		
325	330	335
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct		1056
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		
340	345	350
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa		1104
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		
355	360	365
aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg		1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		
370	375	380

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1178

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 20               25               30  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35               40               45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50               55               60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Ala Ser Ile Asp Glu Leu  
 65               70               75               80  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85               90               95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100              105              110  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115              120              125  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130              135              140  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145              150              155              160  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165              170              175  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
 180              185              190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
 195              200              205  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
 210              215              220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
 225              230              235              240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
 245              250              255  
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
 260              265              270

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 Concord, Massachusetts 01742-9133

Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly  
 275 280 285  
 Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys  
 290 295 300  
 Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn  
 305 310 315 320  
 Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His  
 325 330 335  
 Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala  
 340 345 350  
 Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu  
 355 360 365  
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met  
 370 375 380  
 Leu Ala Asn Ser Val Lys Glu Leu  
 385 390

<210> 75  
 <211> 1178  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1178)

<400> 75  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
  
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
  
 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60  
  
 ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80

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gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288		
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala			
85	90	95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336		
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser			
100	105	110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384		
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys			
115	120	125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432		
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys			
130	135	140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480		
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp			
145	150	155	160
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528		
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly			
165	170	175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576		
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys			
180	185	190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624		
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro			
195	200	205	
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat	672		
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn			
210	215	220	
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720		
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys			
225	230	235	240
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag	768		
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu			
245	250	255	

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acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag	816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys	
260	265
270	
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca	864
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser	
275	280
285	
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta	912
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu	
290	295
300	
aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag	960
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys	
305	310
315	320
caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg	1008
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val	
325	330
335	
ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta	1056
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu	
340	345
350	
aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta	1104
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu	
355	360
365	
ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa	1152
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys	
370	375
380	
aat gct gtt aaa gag ctt aca agt cc	1178
Asn Ala Val Lys Glu Leu Thr Ser	
385	390
<210> 76	
<211> 392	
<212> PRT	
<213> ospC Chimera	
<400> 76	
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1	5
10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20	25
30	

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Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
     35                        40                        45  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val  
     50                        55                        60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
     65                        70                        75                        80  
  
 Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala  
     85                        90                        95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
     100                       105                       110  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
     115                       120                       125  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
     130                       135                       140  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
     145                       150                       155                       160  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
     165                       170                       175  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
     180                       185                       190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
     195                       200                       205  
 Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn  
     210                       215                       220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
     225                       230                       235                       240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
     245                       250                       255  
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
     260                       265                       270  
 Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser  
     275                       280                       285  
 Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu  
     290                       295                       300  
 Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys  
     305                       310                       315                       320  
 Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val  
     325                       330                       335  
 Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu  
     340                       345                       350  
 Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
     355                       360                       365  
 Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys  
     370                       375                       380  
 Asn Ala Val Lys Glu Leu Thr Ser  
     385                       390

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&lt;210&gt; 77

&lt;211&gt; 1230

&lt;212&gt; DNA

&lt;213&gt; ospC Chimera

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1230)

&lt;400&gt; 77

atg	aga	tta	tta	ata	gga	ttt	gct	tta	gcg	tta	gct	tta	ata	gga	tgt	48
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys	
1		5						10					15			

gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
20							25					30				

gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	aaa	ggg	cct	144
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
35						40						45			

aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gcg	gtt	tta	192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	
50						55						60				

ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	ttg	ctg	tca	tct	ata	gat	gaa	att	240
Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	
65						70						75			80	

gct	gct	aaa	gct	att	ggt	aaa	aaa	ata	cac	caa	aat	aat	ggt	ttg	gat	288
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp		
85							90					95				

acc	gaa	tat	aat	cac	aat	gga	tca	ttg	tta	gcg	gga	gct	tat	gca	ata	336
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	
100						105						110				

tca	acc	cta	ata	aaa	caa	aaa	tta	gat	gga	ttg	aaa	aat	gaa	gga	tta	384
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	
115							120					125				

aag	gaa	aaa	att	gat	gcg	gct	aag	aaa	tgt	tct	gaa	aca	ttt	act	aat	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat			480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa			528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
ggc gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca			576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc			624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca			672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser			
210	215	220	
ggc ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct			720
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro			
225	230	235	240
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta			768
Asn Leu Thr Val Ile Ser Lys Ile Thr Asp Ser Asn Ala Phe Leu			
245	250	255	
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt			816
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu			
260	265	270	
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac			864
Ser Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn			
275	280	285	
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca			912
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser			
290	295	300	
aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag			960
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys			
305	310	315	320

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aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag	1008
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys	
325	330
335	
cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat	1056
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp	
340	345
350	
aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt	1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly	
355	360
365	
gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa	1152
Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys	
370	375
380	
gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct	1200
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro	
385	390
395	400
gtt gtg gca gaa agt cca aaa aaa cct taa	1230
Val Val Ala Glu Ser Pro Lys Lys Pro *	
405	

<210> 78  
<211> 409  
<212> PRT  
<213> ospC Chimera

<400> 78			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser  
 210 215 220  
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro  
 225 230 235 240  
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu  
 245 250 255  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 260 265 270  
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn  
 275 280 285  
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser  
 290 295 300  
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys  
 305 310 315 320  
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys  
 325 330 335  
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp  
 340 345 350  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly  
 355 360 365  
 Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys  
 370 375 380  
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro  
 385 390 395 400  
 Val Val Ala Glu Ser Pro Lys Lys Pro  
 405

<210> 79  
 <211> 1209  
 <212> DNA  
 <213> ospC Chimera  
  
 <220>  
 <221> CDS  
 <222> (1)...(1209)

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<400> 79  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175

ggg gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576

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Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser		
180	185	190
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624	
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser		
195	200	205
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672	
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser		
210	215	220
ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720	
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys		
225	230	235
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768	
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala		
245	250	255
gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat	816	
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp		
260	265	270
gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta	864	
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu		
275	280	285
gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta	912	
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu		
290	295	300
att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga	960	
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly		
305	310	315
gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt	1008	
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe		
325	330	335
act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt	1056	
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val		
340	345	350
act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa	1104	
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys		
355	360	365

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act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac		1152
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn		
370	375	380
ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt		1200
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu		
385	390	395
aca agc taa		1209
Thr Ser *		
<210> 80		
<211> 402		
<212> PRT		
<213> ospC Chimera		
<400> 80		
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys		
1 5 10 15		
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys		
20 25 30		
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro		
35 40 45		
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu		
50 55 60		
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile		
65 70 75 80		
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp		
85 90 95		
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile		
100 105 110		
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu		
115 120 125		
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn		
130 135 140		
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp		
145 150 155 160		
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys		
165 170 175		
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser		
180 185 190		
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser		
195 200 205		
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser		
210 215 220		

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Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 225 230 235 240  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
 245 250 255  
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
 260 265 270  
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu  
 275 280 285  
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
 290 295 300  
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
 305 310 315 320  
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
 325 330 335  
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
 340 345 350  
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys  
 355 360 365  
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
 370 375 380  
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu  
 385 390 395 400  
 Thr Ser

<210> 81  
 <211> 1205  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1205)

<400> 81  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45

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aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192		
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240		
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288		
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336		
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384		
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432		
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480		
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528		
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576		
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624		
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672		
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser			
210	215	220	
gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720		
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys			
225	230	235	240

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ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala	
245	250
255	
gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat	816
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp	
260	265
270	
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt	864
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly	
275	280
285	
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat	912
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr	
290	295
300	
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca	960
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser	
305	310
320	
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat	1008
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp	
325	330
335	
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat	1056
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn	
340	345
350	
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct	1104
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala	
355	360
365	
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa	1152
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu	
370	375
380	
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag	1200
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu	
385	390
395	400
ctt ac	1205
Leu	

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<210> 82  
<211> 401  
<212> PRT  
<213> ospC Chimera

<400> 82  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
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Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80  
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175  
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
180 185 190  
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
195 200 205  
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
210 215 220  
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
225 230 235 240  
Gly Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala  
245 250 255  
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp  
260 265 270  
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly  
275 280 285  
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr  
290 295 300  
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser  
305 310 315 320

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Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp  
                  325                 330                 335  
 Phe Thr Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn  
                  340                 345                 350  
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala  
                  355                 360                 365  
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu  
                  370                 375                 380  
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu  
                  385                 390                 395                 400  
 Leu

<210> 83  
 <211> 1236  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1236)

<400> 83

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1                       5                         10                     15	
gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys	
20                     25                         30	
ggg ggt gat tct gca tct act aat cct gct gac gag tct gct ggg aaa	144
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly	
35                     40                         45	
cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt	192
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe	
50                     55                         60	
gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa	240
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu	
65                     70                         75                     80	
ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta	288
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu	
85                     90                         95	

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gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala 100 105 110	336
ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 115 120 125	384
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 130 135 140	432
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 145 150 155 160	480
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr 165 170 175	528
gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly 180 185 190	576
ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu 195 200 205	624
aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn 210 215 220	672
aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys 225 230 235 240	720
gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala 245 250 255	768
ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp 260 265 270	816
gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu 275 280 285	864

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gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa	912
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu	
290	295
	300
ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa	960
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu	
305	310
	315
320	
tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act	1008
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr	
325	330
	335
act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag	1056
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln	
340	345
	350
gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac	1104
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp	
355	360
	365
aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg	1152
Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu	
370	375
	380
tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca	1200
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr	
385	390
	395
	400
aat cct gtt gtg gca gaa agt cca aaa aaa cct taa	1236
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	
405	410
<210> 84	
<211> 411	
<212> PRT	
<213> ospC Chimera	
<400> 84	
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys	
20 25 30	
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly	
35 40 45	

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Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
       50                  55                  60  
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu  
  65                  70                  75                  80  
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu  
       85                  90                  95  
 Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala  
       100                105                110  
 Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu  
       115                120                125  
 Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe  
       130                135                140  
 Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala  
  145                150                155                160  
 Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr  
       165                170                175  
 Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly  
       180                185                190  
 Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu  
       195                200                205  
 Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn  
       210                215                220  
 Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys  
  225                230                235                240  
 Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala  
       245                250                255  
 Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp  
       260                265                270  
 Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu  
       275                280                285  
 Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu  
       290                295                300  
 Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu  
  305                310                315                320  
 Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr  
       325                330                335  
 Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln  
       340                345                350  
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp  
       355                360                365  
 Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu  
       370                375                380  
 Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr  
  385                390                395                400  
  
 Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
       405                410

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<210> 85  
<211> 192  
<212> PRT  
<213> borrelia burgdorferi

<400> 85

Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp
1				5					10				15		
Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr
					20			25					30		
Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu
					35			40				45			
Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn
					50			55			60				
Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser
					65			70			75			80	
Gly	Ala	Tyr	Leu	Ile	Ser	Thr	Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile
					85			90			95				
Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys
					100			105			110				
Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr	Asp	Leu	Gly
					115			120			125				
Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr
					130			135			140				
Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp	Glu	Leu	Glu	Lys	Leu	Phe	Glu
					145			150			155			160	
Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Thr	Asn	Ser
					165			170			175				
Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro
					180			185			190				

<210> 86  
<211> 191  
<212> PRT  
<213> borrelia burgdorferi

<400> 86

Asn	Ser	Gly	Lys	Gly	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser
1					5				10			15			
Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser
					20			25			30				
Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Ala	Ser	
					35			40			45				

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Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn		
50	55	60
Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly		
65	70	75
Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys		
85	90	95
Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser		
100	105	110
Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile		
115	120	125
Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp		
130	135	140
Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala		
145	150	155
Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val		
165	170	175
Lys Glu Leu Thr Ser Pro Ile Val Ala Glu Ser Pro Lys Lys Pro		
180	185	190

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UNITED STATES PATENT AND TRADEMARK OFFICE  
**CERTIFICATE OF CORRECTION**

PATENT NO. : **7,060,281 B1**  
DATED : **June 13, 2006**  
INVENTOR(S) : **Raymond J. Dattwyler, Gerald Steinost, Daniel Dykhuizen, Benjamin J. Luft, Maria J.C. Gomes-Solecki**

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

**At Column 45, Insert SEQ ID NOS. 53-86 after SEQ ID NO: 52**

<210> 53

<211> 1137

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1137)

<400> 53

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48  
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser  
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96  
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192

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PATENT NO. **7,060,281 B1**

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Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	
50							55				60					
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tta	gca	gga	gct	tat	aca	ata	tca	acc	tta	ata	aca	caa	aaa	tta	agt	288
Leu	Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Thr	Leu	Ile	Thr	Gln	Lys	Leu	Ser	
85						90				95						
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Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys	
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aaa	tgc	tct	gaa	gag	ttt	agt	act	aaa	cta	aaa	gat	aat	cat	gca	cag	384
Lys	Cys	Ser	Glu	Glu	Phe	Ser	Thr	Lys	Leu	Lys	Asp	Asn	His	Ala	Gln	
115						120				125						
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Leu	Gly	Ile	Gln	Gly	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	
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145						150				155			160			
ttg	tcc	gga	tca	tta	gaa	agc	tta	tca	aaa	gca	gct	aaa	gag	atg	ctt	528
Leu	Ser	Gly	Ser	Leu	Glu	Ser	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	
165						170				175						
gct	aat	tca	gtt	aaa	gag	ctt	aca	agc	cct	gtt	gtc	cat	ggt	aat	aat	576
Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	His	Gly	Asn	Asn	
180						185				190						
tca	ggg	gat	tct	gca	tct	act	aat	cct	gat	gag	tct	gca	aaa	gga		624
Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	
195						200				205						
cct	aat	ctt	acc	gta	ata	agc	aaa	aaa	att	aca	gat	tct	aat	gca	ttt	672
Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	
210						215				220						
tta	ctg	gct	gtg	aaa	gaa	gtt	gag	gct	ttg	ctt	tca	tct	ata	gat	gaa	720
Leu	Leu	Ala	Val	Lys	Glu	Val	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu		
225						230				235			240			

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ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp	245	250	255	768
aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile	260	265	270	816
tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu	275	280	285	864
aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr	290	295	300	912
aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp	305	310	315	960
320				
gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys	325	330	335	1008
340				
ggg gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser	345	350	350	1056
355				
aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn	360	365	365	1104
370				
cct gtt gtg gca gaa agt cca aaa aaa cct taa Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	375			1137

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<213> ospC Chimera

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20               25                           30  
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala  
35               40                           45  
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile  
50               55                           60  
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu  
65               70                           75                           80  
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser  
85               90                           95  
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys  
100              105                           110  
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln  
115              120                           125  
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu  
130              135                           140  
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys  
145              150                           155                           160  
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu  
165              170                           175  
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn  
180              185                           190  
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly  
195              200                           205  
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
210              215                           220  
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu  
225              230                           235                           240  
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp  
245              250                           255  
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile  
260              265                           270  
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu  
275              280                           285  
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr  
290              295                           300  
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp  
305              310                           315                           320

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Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys		
325	330	335
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser		
340	345	350
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn		
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Pro Val Val Ala Glu Ser Pro Lys Lys Pro		
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		15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa		
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	96	
20	25	30
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg		
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	144	
35	40	45
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa		
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	192	
50	55	60
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca		
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	240	
65	70	75
		80
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta		
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	288	
85	90	95

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gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 180 185 190	576
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn 195 200 205	624
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys 210 215 220	672
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala 225 230 235 240	720
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile 245 250 255	768
aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 260 265 270	816
ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser 275 280 285	864

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gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat		912
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp		
290	295	300
tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt		960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu		
305	310	315
320		
ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa		1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys		
325	330	335
aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt		1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe		
340	345	350
aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat		1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Leu Thr Asn		
355	360	365
tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa		1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys		
370	375	380
cct taa		1158
Pro *		
385		
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys		
20 25 30		
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala		
35 40 45		
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys		
50 55 60		
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser		
65 70 75 80		

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Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu
							85			90					95
Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys
							100			105					110
Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	Lys	Leu	Lys	Glu	Lys	His	Thr	Asp
							115			120					125
Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu
							130			135					140
Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys	Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu
							145			150					160
Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala
							165			170					175
Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys
							180			185					190
Lys	Pro	Phe	His	Gly	Asn	Asn	Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn
							195			200					205
Pro	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	Lys
							210			215					220
Ile	Thr	Asp	Ser	Asn	Ala	Phe	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala
							225			230					240
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ser	Lys	Ala	Ile	Gly	Lys	Lys	Ile
							245			250					255
Lys	Asn	Asp	Gly	Thr	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu
							260			265					270
Ile	Ala	Gly	Ala	Tyr	Glu	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Ser
							275			280					285
Val	Leu	Asn	Ser	Glu	Glu	Leu	Lys	Lys	Ile	Lys	Glu	Ala	Lys	Asp	
							290			295					300
Cys	Ser	Gln	Lys	Phe	Thr	Thr	Lys	Leu	Lys	Asp	Ser	His	Ala	Glu	Leu
							305			310					320
Gly	Ile	Gln	Ser	Val	Gln	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys
							325			330					335
Thr	His	Gly	Thr	Lys	Asp	Lys	Gly	Ala	Lys	Glu	Leu	Glu	Glu	Leu	Phe
							340			345					350
Lys	Ser	Leu	Glu	Ser	Leu	Ser	Lys	Ala	Ala	Gln	Ala	Ala	Leu	Thr	Asn
							355			360					365
Ser	Val	Lys	Glu	Leu	Thr	Asn	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys
							370			375					380

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Pro  
385

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gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 96  
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys  
20 25 30

att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 144  
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr  
35 40 45

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 192  
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys  
50 55 60

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 240  
Ile Asp Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser  
65 70 75 80

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 288  
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu  
85 90 95

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 336  
Ser Lys Leu Lys Asn Leu Glu Leu Lys Thr Glu Ile Ala Lys Ala  
100 105 110

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 384  
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala  
115 120 125

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att 432

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Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile			
130	135	140	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat			480
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp			
145	150	155	160
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta			528
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu			
165	170	175	
act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca			576
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro			
180	185	190	
aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act			624
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr			
195	200	205	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa			672
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys			
210	215	220	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag			720
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu			
225	230	235	240
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa			768
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys			
245	250	255	
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca			816
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser			
260	265	270	
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta			864
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu			
275	280	285	
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag			912
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys			
290	295	300	
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag			960
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu			
305	310	315	320

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ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta		1008
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu		
325	330	335
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta		1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu		
340	345	350
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act		1104
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr		
355	360	365
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa		1152
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys		
370	375	380
aaa cct taa		1161
Lys Pro *		
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20 25 30		
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr		
35 40 45		
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys		
50 55 60		
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser		
65 70 75 80		
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu		
85 90 95		
Ser Lys Leu Lys Asn Leu Glu Leu Lys Thr Glu Ile Ala Lys Ala		
100 105 110		
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala		
115 120 125		
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile		
130 135 140		

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Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp  
 145 150 155 160  
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu  
 165 170 175  
 Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro  
 180 185 190  
 Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
 195 200 205  
 Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
 210 215 220  
 Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
 225 230 235 240  
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
 245 250 255  
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
 260 265 270  
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
 275 280 285  
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys  
 290 295 300  
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
 305 310 315 320  
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
 325 330 335  
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
 340 345 350  
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
 355 360 365  
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
 370 375 380  
 Lys Pro  
 385

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021005

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 Concord, Massachusetts 01742-9133

```

<210> 59
<211> 1197
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1197)

<400> 59
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt      48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1           5           10           15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa      96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20          25          30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct      144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35          40          45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta      192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50          55          60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att      240
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65          70          75          80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat      288
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp
 85          90          95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata      336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100         105         110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta      384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115         120         125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat      432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130         135         140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat      480

```

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Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp				
145	150	155	160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa				528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys				
165	170	175		
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca				576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser				
180	185	190		
aaa gca gct,aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc				624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser				
195	200	205		
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat				672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp				
210	215	220		
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat				720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn				
225	230	235	240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc				768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu				
245	250	255		
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct				816
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala				
260	265	270		
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag				864
Lys Ala Ile Gly Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu				
275	280	285		
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac				912
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn				
290	295	300		
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag				960
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys				
305	310	315	320	
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa				1008
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys				
325	330	335		

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tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056  
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
 340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
 355 360 365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152  
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
 370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197  
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390 395

<210> 60  
<211> 399  
<212> PRT  
<213> ospC Chimera

<400> 60  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190

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Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
           195                  200                  205  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
           210                  215                  220  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
           225                  230                  235                  240  
  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
           245                  250                  255  
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala  
           260                  265                  270  
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu  
           275                  280                  285  
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn  
           290                  295                  300  
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys  
           305                  310                  315                  320  
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys  
           325                  330                  335  
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp  
           340                  345                  350  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly  
           355                  360                  365  
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys  
           370                  375                  380  
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
           385                  390                  395

<210> 61  
 <211> 1196  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1196)

<400> 61  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
   1              5                  10                  15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa   96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
   20                  25                  30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct		144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro		
35	40	45
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta		192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu		
50	55	60
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att		240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile		
65	70	75
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat		288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp		
85	90	95
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata		336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile		
100	105	110
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta		384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu		
115	120	125
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat		432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn		
130	135	140
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat		480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp		
145	150	155
160		
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa		528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys		
165	170	175
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca		576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser		
180	185	190
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc		624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser		
195	200	205
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat		672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp		
210	215	220

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&lt;210&gt; 62

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; ospC Chimera

&lt;400&gt; 62

Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Leu Ile Gly Cys  
 1               5   10   15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20   25   30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35   40   45  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50   55   60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65   70   75   80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp  
 85   90   95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100   105   110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115   120   125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130   135   140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145   150   155   160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165   170   175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180   185   190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195   200   205  
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp  
 210   215   220  
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn  
 225   230   235   240  
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu  
 245   250   255  
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala  
 260   265   270  
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val  
 275   280   285  
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 290   295   300  
 Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu  
 305   310   315   320

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Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	Asp	Phe	Thr	Lys
325							330								335

  

Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	Asn	Val	Thr	Asp
340							345								350

  

Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp	Ala	Ala	Lys	Asp	Lys
355							360							365	

  

Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ala
370							375							380	

  

Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu		
385							390							395	

&lt;210&gt; 63

&lt;211&gt; 1185

&lt;212&gt; DNA

&lt;213&gt; ospC Chimera

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1185)

&lt;400&gt; 63

atg	aga	tta	tta	ata	gga	ttt	gct	tta	gct	tta	ata	gga	tgt		48	
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys	
1				5					10				15			

gca	caa	aaa	ggg	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
20				25									30			

gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	144
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	
35				40						45						

aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gct	gtt	tta	192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	
50				55						60						

ctt	gct	gtg	aaa	gag	gtt	gaa	gct	ttg	ctg	tca	tct	ata	gat	gag	ctt	240
Leu	Ala	Val	Lys	Glu	Val	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu		
65				70				75				80				

gct	aaa	gct	att	ggt	aaa	aaa	ata	aaa	aac	gat	ggt	agt	tta	gat	aat	288
Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn	
85				90									95			

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser 100 105 110	336
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu 115 120 125	384
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr 130 135 140	432
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp 145 150 155 160	480
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp 165 170 175	528
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu 180 185 190	576
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser 210 215 220	672
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly 260 265 270	816
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac	864
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 Concord, Massachusetts 01742-9133

Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn			
275	280	285	
gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa			912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys			
290	295	300	
aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa			960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu			
305	310	315	320
aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa			1008
Lys Ala Lys Lys Cys Ser Gly Glu Phe Thr Ala Lys Leu Lys Gly Glu			
325	330	335	
cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa			1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys			
340	345	350	
gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt			1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu			
355	360	365	
gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag			1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu			
370	375	380	
atg ctt act aat tca gtt aaa gag ctt aca agc			1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser			
385	390	395	

<210> 64  
<211> 395  
<212> PRT  
<213> ospC Chimera

<400> 64			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	

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Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 100 105 110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
 130 135 140  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
 145 150 155 160  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
 165 170 175  
 Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
 180 185 190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
 195 200 205  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
 210 215 220  
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
 225 230 235 240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
 245 250 255  
 Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly  
 260 265 270  
 Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn  
 275 280 285  
 Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys  
 290 295 300  
 Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu  
 305 310 315 320  
 Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu  
 325 330 335  
 His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys  
 340 345 350  
 Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu  
 355 360 365  
 Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu  
 370 375 380  
 Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390 395

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<210> 65  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera  
  
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 <221> CDS  
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 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
  
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
  
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65 70 75 80  
  
 gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95  
  
 gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 100 105 110  
  
 acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
 115 120 125  
  
 aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
 130 135 140  
  
 aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480

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Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat			528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta			576
Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu			
180	185	190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca			624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr			
195	200	205	
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct			672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser			
210	215	220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata			720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile			
225	230	235	240
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa			768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu			
245	250	255	
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att			816
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile			
260	265	270	
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat			864
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His			
275	280	285	
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca			912
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr			
290	295	300	
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att			960
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile			
305	310	315	320
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga			1008
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly			
325	330	335	

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gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa 1056  
 Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys  
 340 345 350

aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag 1104  
 Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu  
 355 360 365

ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa 1152  
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys  
 370 375 380

gag atg ctt gct aat tca gtt aaa gag ctt ac 1184  
 Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
 385 390

<210> 66  
 <211> 394  
 <212> PRT  
 <213> ospC Chimera

<400> 66  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 100 105 110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
 130 135 140  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
 145 150 155 160  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
 165 170 175

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Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
     180                        185                        190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
     195                        200                        205  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser  
     210                        215                        220  
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
     225                        230                        235                        240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
     245                        250                        255  
 Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
     260                        265                        270  
 Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His  
     275                        280                        285  
 Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr  
     290                        295                        300  
 Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile  
     305                        310                        315                        320  
 Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly  
     325                        330                        335  
 Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys  
     340                        345                        350  
 Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu  
     355                        360                        365  
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys  
     370                        375                        380  
 Glu Met Leu Ala Asn Ser Val Lys Glu Leu  
     385                        390

<210> 67  
 <211> 1184  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1184)

<400> 67  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
     1                       5                               10                       15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa   96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
     20                       25                               30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35	40
45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50	55
60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65	70
75	80
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85	90
95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100	105
110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115	120
125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130	135
140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145	150
155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165	170
175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180	185
190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195	200
205	

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agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser	
210	215
	220
aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225	230
	235
240	
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245	250
	255
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att	816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
260	265
	270
ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac	864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn	
275	280
	285
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa	912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu	
290	295
	300
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca	960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr	
305	310
	315
320	
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat	1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His	
325	330
	335
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct	1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala	
340	345
	350
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa	1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355	360
	365
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr	
370	375
	380
tta aaa aat gct gtt aaa gag ctt aca agt cc	1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser	
385	390

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<210> 68  
 <211> 394  
 <212> PRT  
 <213> ospC Chimera

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
 85 90 95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
 100 105 110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
 130 135 140  
  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
 145 150 155 160  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
 165 170 175  
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
 180 185 190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
 195 200 205  
 Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser  
 210 215 220  
 Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile  
 225 230 235 240  
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu  
 245 250 255  
 Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile  
 260 265 270  
 Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn  
 275 280 285  
 Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu  
 290 295 300

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Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr  
 305 310 315 320  
 Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His  
 325 330 335  
 Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala  
 340 345 350  
 Ile Leu Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu  
 355 360 365  
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr  
 370 375 380  
 Leu Lys Asn Ala Val Lys Glu Leu Thr Ser  
 385 390

<210> 69  
<211> 1209  
<212> DNA  
<213> ospC Chimera

<220>  
<221> CDS  
<222> (1)...(1209)

<400> 69  
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15  
  
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30  
  
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45  
  
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60  
  
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240  
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu  
65 70 75 80  
  
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt aat gat aat 288  
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
85 90 95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100	105
	110
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115	120
	125
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130	135
	140
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145	150
	155
	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165	170
	175
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180	185
	190
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195	200
	205
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
210	215
	220
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
225	230
	235
	240
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
245	250
	255
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
260	265
	270

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ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser 275 280 285	864
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu 290 295 300	912
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys 305 310 315 320	960
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu 325 330 335	1008
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu 340 345 350	1056
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu 355 360 365	1104
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr 370 375 380	1152
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys 385 390 395 400	1200
aaa cct taa Lys Pro *	1209
<210> 70 <211> 402 <212> PRT <213> ospC Chimera	
<400> 70 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 1 5 10 15 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 20 25 30	

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Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
                   35                  40                  45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
       50                  55                  60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
   65                  70                  75                  80  
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn  
       85                  90                  95  
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser  
       100                  105                  110  
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu  
       115                  120                  125  
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr  
       130                  135                  140  
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp  
   145                  150                  155                  160  
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp  
       165                  170                  175  
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu  
       180                  185                  190  
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr  
       195                  200                  205  
 Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr  
       210                  215                  220  
 Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys  
   225                  230                  235                  240  
 Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu  
       245                  250                  255  
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys  
       260                  265                  270  
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser  
       275                  280                  285  
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu  
       290                  295                  300  
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys  
   305                  310                  315                  320  
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu  
       325                  330                  335  
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu  
       340                  345                  350  
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu  
       355                  360                  365  
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr  
       370                  375                  380  
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys  
   385                  390                  395                  400  
 Lys Pro

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<211> 1179
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
    1           5           10          15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
    20          25          30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
    35          40          45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
    50          55          60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
    65          70          75          80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala
    85          90          95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
    100         105         110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
    115         120         125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
    130         135         140

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cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat		480	
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp			
145	150	155	160
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt		528	
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly			
165	170	175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa		576	
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys			
180	185	190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct		624	
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro			
195	200	205	
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat		672	
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn			
210	215	220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa		720	
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys			
225	230	235	240
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa		768	
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu			
245	250	255	
act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa		816	
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys			
260	265	270	
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca		864	
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser			
275	280	285	
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata		912	
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile			
290	295	300	
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct		960	
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala			
305	310	315	320
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca		1008	
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr			
325	330	335	

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gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056  
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
 340 345 350

tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104  
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
 355 360 365

tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152  
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
 370 375 380

act aat tca gtt aaa gag ctt aca agc 1179  
 Thr Asn Ser Val Lys Glu Leu Thr Ser  
 385 390

<210> 72  
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 <212> PRT  
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 20 25 30  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val  
 50 55 60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65 70 75 80  
 Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85 90 95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100 105 110  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115 120 125  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130 135 140  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145 150 155 160  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165 170 175

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Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
                  180                 185                 190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
                  195                 200                 205  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
                  210                 215                 220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
                  225                 230                 235                 240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
                  245                 250                 255  
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys  
                  260                 265                 270  
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser  
                  275                 280                 285  
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile  
                  290                 295                 300  
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala  
                  305                 310                 315                 320  
 Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr  
                  325                 330                 335

Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile  
                  340                 345                 350  
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys  
                  355                 360                 365  
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu  
                  370                 375                 380  
 Thr Asn Ser Val Lys Glu Leu Thr Ser  
                  385                 390

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 <212> DNA  
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<400> 73  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
  1             5                 10                 15

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gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	20	25	30	96
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	35	40	45	144
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	50	55	60	192
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	65	70	75	240
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	85	90	95	288
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	100	105	110	336
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	115	120	125	384
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	130	135	140	432
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	145	150	155	480
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	165	170	175	528
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	180	185	190	576
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	195	200	205	624

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att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn 210 215 220	672
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu 245 250 255	768
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys 260 265 270	816
aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly 275 280 285	864
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys 290 295 300	912
•tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn 305 310 315 320	960
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His 325 330 335	1008
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala 340 345 350	1056
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu 355 360 365	1104
aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met 370 375 380	1152

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ctt gct aat tca gtt aaa gag ctt ac  
 Leu Ala Asn Ser Val Lys Glu Leu  
 385                   390

1178

<210> 74  
 <211> 392  
 <212> PRT  
 <213> ospC Chimera

<400> 74  
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 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20               25                   30  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35               40                   45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
 50               55                   60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
 65               70                   75                   80  
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala  
 85               90                   95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
 100              105                   110  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
 115              120                   125  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
 130              135                   140  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
 145              150                   155                   160  
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly  
 165              170                   175  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
 180              185                   190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
 195              200                   205  
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn  
 210              215                   220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
 225              230                   235                   240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu  
 245              250                   255  
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
 260              265                   270

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Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly  
     275                  280                  285  
 Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys  
     290                  295                  300  
 Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn  
     305                  310                  315                  320  
 Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His  
     325                  330                  335  
 Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala  
     340                  345                  350  
 Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu  
     355                  360                  365  
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met  
     370                  375                  380  
 Leu Ala Asn Ser Val Lys Glu Leu  
     385                  390

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 <212> DNA  
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
     1                  5                  10                  15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa    96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
     20                  25                  30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct    144  
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
     35                  40                  45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt    192  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
     50                  55                  60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt    240  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
     65                  70                  75                  80

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gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala 85 90 95	288
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser 100 105 110	336
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys 115 120 125	384
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys 130 135 140	432
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asn Leu Thr Asp Asp 145 150 155 160	480
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys Gly 165 170 175	528
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys 180 185 190	576
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro 195 200 205	624
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn 210 215 220	672
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu 245 250 255	768

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acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag	816		
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys			
260	265	270	
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca	864		
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser			
275	280	285	
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta	912		
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu			
290	295	300	
aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag	960		
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys			
305	310	315	320
caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg	1008		
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val			
325	330	335	
ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta	1056		
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu			
340	345	350	
aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta	1104		
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu			
355	360	365	
ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa	1152		
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys			
370	375	380	
aat gct gtt aaa gag ctt aca agt cc	1178		
Asn Ala Val Lys Glu Leu Thr Ser			
385	390		
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Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20 25 30			

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Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
           35                  40                  45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val  
       50                  55                  60  
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu  
   65                  70                  75                  80  
  
 Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala  
       85                  90                  95  
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser  
       100                  105                  110  
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys  
       115                  120                  125  
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys  
       130                  135                  140  
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp  
   145                  150                  155                  160  
 Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys Gly  
       165                  170                  175  
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys  
       180                  185                  190  
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro  
       195                  200                  205  
 Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn  
       210                  215                  220  
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys  
       225                  230                  235                  240  
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu  
       245                  250                  255  
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys  
       260                  265                  270  
 Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser  
       275                  280                  285  
 Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu  
       290                  295                  300  
 Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys  
       305                  310                  315                  320  
 Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val  
       325                  330                  335  
 Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu  
       340                  345                  350  
 Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu  
       355                  360                  365  
 Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys  
       370                  375                  380  
 Asn Ala Val Lys Glu Leu Thr Ser  
       385                  390

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&lt;210&gt; 77

&lt;211&gt; 1230

&lt;212&gt; DNA

&lt;213&gt; ospC Chimera

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1230)

&lt;400&gt; 77

atg	aga	tta	tta	ata	gga	ttt	gct	tta	gcg	tta	gct	tta	ata	gga	tgt	48
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys	
1		5						10					15			

gca	caa	aaa	ggg	aat	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Asn	Gly	Lys		
20					25								30					

gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	144	
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro		
35					40							45					

aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gct	gtt	tta	192	
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu		
50					55							60					

ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	ttg	ctg	tca	tct	ata	gat	gaa	att	240
Leu	Ala	Val	Lys	Glu	Val	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile		
65				70							75		80			

gct	gct	aaa	gct	att	ggt	aaa	aaa	ata	cac	caa	aat	aat	ggt	ttg	gat	288
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp		
85					90						95					

acc	gaa	tat	aat	cac	aat	gga	tca	ttg	tta	gcg	gga	gct	tat	gca	ata	336
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	
100					105							110				

tca	acc	cta	ata	aaa	caa	aaa	tta	gat	gga	ttg	aaa	aat	gaa	gga	tta	384
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	
115					120						125					

aag	gaa	aaa	att	gat	gcg	gct	aag	aaa	tgt	tct	gaa	aca	ttt	act	aat	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat			480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa			528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
ggg gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca			576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc			624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca			672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser			
210	215	220	
ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct			720
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro			
225	230	235	240
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta			768
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu			
245	250	255	
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt			816
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu			
260	265	270	
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac			864
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn			
275	280	285	
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca			912
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser			
290	295	300	
aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag			960
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys			
305	310	315	320

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aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag 1008  
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys  
                   325                  330                  335  
  
 cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat 1056  
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp  
                   340                  345                  350  
  
 aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt 1104  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly  
                   355                  360                  365  
  
 gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa 1152  
 Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys  
                   370                  375                  380  
  
 gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct 1200  
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro  
                   385                  390                  395                  400  
  
 gtt gtg gca gaa agt cca aaa aaa cct taa 1230  
 Val Val Ala Glu Ser Pro Lys Lys Pro \*  
                   405  
  
 <210> 78  
 <211> 409  
 <212> PRT  
 <213> ospC Chimera  
  
 <400> 78  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 50 55 60  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 115 120 125

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser  
 210 215 220  
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro  
 225 230 235 240  
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu  
 245 250 255  
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu  
 260 265 270  
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn  
 275 280 285  
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser  
 290 295 300  
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys  
 305 310 315 320  
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys  
 325 330 335  
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp  
 340 345 350  
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly  
 355 360 365  
 Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys  
 370 375 380  
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro  
 385 390 395 400  
 Val Val Ala Glu Ser Pro Lys Lys Pro  
 405

<210> 79  
 <211> 1209  
 <212> DNA  
 <213> ospC Chimera  
  
 <220>  
 <221> CDS  
 <222> (1)...(1209)

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<400> 79  
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48  
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96  
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144  
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192  
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu  
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240  
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile  
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288  
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp  
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336  
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384  
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432  
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480  
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aat aaa act aaa 528  
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576

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Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc			624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca			672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser			
210	215	220	
ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa			720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys			
225	230	235	240
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca			768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala			
245	250	255	
gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat			816
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp			
260	265	270	
gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta			864
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu			
275	280	285	
gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta			912
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu			
290	295	300	
att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga			960
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly			
305	310	315	320
gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt			1008
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe			
325	330	335	
act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt			1056
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val			
340	345	350	
act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa			1104
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys			
355	360	365	

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act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac		1152	
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn			
370	375	380	
ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt		1200	
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu			
385	390	395	
aca agc taa		1209	
Thr Ser *			
<210> 80			
<211> 402			
<212> PRT			
<213> ospC Chimera			
<400> 80			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser			
210	215	220	

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Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 225                   230                   235                   240  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala  
 245                   250                   255  
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp  
 260                   265                   270  
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu  
 275                   280                   285  
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu  
 290                   295                   300  
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly  
 305                   310                   315                   320  
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe  
 325                   330                   335  
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val  
 340                   345                   350  
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys  
 355                   360                   365  
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn  
 370                   375                   380  
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu  
 385                   390                   395                   400  
 Thr Ser

<210> 81  
 <211> 1205  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1205)

<400> 81  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt     48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1               5               10               15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa     96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20              25              30  
  
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct     144  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35              40              45

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aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50	55
55	60
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65	70
70	75
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85	90
90	95
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100	105
105	110
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115	120
120	125
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130	135
135	140
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145	150
150	155
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165	170
170	175
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180	185
185	190
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195	200
200	205
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser	
210	215
215	220
gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys	
225	230
230	235
240	240

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ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 245 250 255	768
gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp 260 265 270	816
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly 275 280 285	864
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr 290 295 300	912
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser 305 310 315 320	960
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp 325 330 335	1008
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn 340 345 350	1056
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala 355 360 365	1104
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu 370 375 380	1152
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag Asn Leu Ala Lys Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu 385 390 395 400	1200
ctt ac Leu	1205

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&lt;210&gt; 82

&lt;211&gt; 401

&lt;212&gt; PRT

&lt;213&gt; ospC Chimera

&lt;400&gt; 82

Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
 1 5 10 15  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys  
 20 25 30  
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro  
 35 40 45  
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu  
 50 55 60  
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile  
 65 70 75 80  
 Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp  
 85 90 95  
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile  
 100 105 110  
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu  
 115 120 125  
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn  
 130 135 140  
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp  
 145 150 155 160  
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys  
 165 170 175  
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser  
 180 185 190  
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser  
 195 200 205  
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser  
 210 215 220  
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys  
 225 230 235 240  
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala  
 245 250 255  
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp  
 260 265 270  
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly  
 275 280 285  
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr  
 290 295 300  
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser  
 305 310 315 320

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Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp  
                   325                  330                  335  
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn  
                   340                  345                  350  
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala  
                   355                  360                  365  
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu  
                   370                  375                  380  
 Asn Leu Ala Lys Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu  
                   385                  390                  395                  400  
 Leu

<210> 83  
 <211> 1236  
 <212> DNA  
 <213> ospC Chimera

<220>  
 <221> CDS  
 <222> (1)...(1236)

<400> 83  
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt   48  
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys  
       1              5                  10                  15  
  
 gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa   96  
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys  
       20                  25                  30  
  
 ggt ggg gat tct gca tct act aat cct gct gac gag tct gcg aaa ggg   144  
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly  
       35                  40                  45  
  
 cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt   192  
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
       50                  55                  60  
  
 gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa   240  
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu  
       65                  70                  75                  80  
  
 ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta   288  
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu  
       85                  90                  95

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gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala 100 105 110	336
ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 115 120 125	384
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 130 135 140	432
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 145 150 155 160	480
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc Thr Asp Asp His Ala Lys Ala Ile Leu Lys Thr His Ala Thr Thr 165 170 175	528
gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly 180 185 190	576
ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu 195 200 205	624
aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn 210 215 220	672
aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys 225 230 235 240	720
gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala 245 250 255	768
ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp 260 265 270	816
gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu 275 280 285	864

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gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa		912	
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu			
290	295	300	
ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa		960	
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu			
305	310	315	
320			
tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act		1008	
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr			
325	330	335	
act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag		1056	
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln			
340	345	350	
gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac		1104	
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp			
355	360	365	
aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg		1152	
Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu			
370	375	380	
tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca		1200	
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr			
385	390	395	
400			
aat cct gtt gtg gca gaa agt cca aaa aaa cct taa		1236	
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *			
405	410		
<210> 84			
<211> 411			
<212> PRT			
<213> ospC Chimera			
<400> 84			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys			
20	25	30	
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly			
35	40	45	

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Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe  
   50                       55                       60  
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu  
   65                       70                       75                       80  
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu  
   85                       90                       95  
 Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala  
  100                      105                      110  
 Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu  
  115                      120                      125  
 Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe  
  130                      135                      140  
 Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala  
  145                      150                      155                      160  
 Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr  
  165                      170                      175  
 Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly  
  180                      185                      190  
 Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu  
  195                      200                      205  
 Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn  
  210                      215                      220  
 Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys  
  225                      230                      235                      240  
 Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala  
  245                      250                      255  
 Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp  
  260                      265                      270  
 Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu  
  275                      280                      285  
 Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu  
  290                      295                      300  
 Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu  
  305                      310                      315                      320  
 Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr  
  325                      330                      335  
 Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln  
  340                      345                      350  
 Asp Asp Asn Ala Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp  
  355                      360                      365  
 Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu  
  370                      375                      380  
 Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr  
  385                      390                      395                      400  
  
 Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro  
  405                      410

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<210> 85  
<211> 192  
<212> PRT  
<213> borrelia burgdorferi

<400> 85

Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp
1				5				10							15
Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr
					20			25							30
Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu
					35			40							45
Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn
					50			55							60
Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser
					65			70			75				80
Gly	Ala	Tyr	Leu	Ile	Ser	Thr	Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile
					85			90							95
Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys
					100			105							110
Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr	Asp	Leu	Gly
					115			120							125
Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr
					130			135							140
Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp	Glu	Leu	Glu	Lys	Leu	Phe	Glu
					145			150			155				160
Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Thr	Asn	Ser
					165			170							175
Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro
					180			185							190

<210> 86  
<211> 191  
<212> PRT  
<213> borrelia burgdorferi

<400> 86

Asn	Ser	Gly	Lys	Gly	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser
1					5			10							15
Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser
					20			25							30
Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser
					35			40							45

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Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Ile Gln Gln Asn  
50 55 60  
Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly  
65 70 75 80  
Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys  
85 90 95  
Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser  
100 105 110  
Glu Asp Phe Thr Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile  
115 120 125  
Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp  
130 135 140  
Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala  
145 150 155 160  
Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val  
165 170 175  
Lys Glu Leu Thr Ser Pro Ile Val Ala Glu Ser Pro Lys Lys Pro  
180 185 190

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